

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lu, Kuang-hui
Pang, Kevin
- (ii) TITLE OF INVENTION: Methods and Reagents for Treating
Glucose Metabolic Disorders
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Foley, Hoag & Eliot
(B) STREET: One Post Office Square
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02109
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: ASCII (text)
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 10-FEB-2000
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Vincent, Matthew P.
(B) REGISTRATION NUMBER: 36,709
(C) REFERENCE/DOCKET NUMBER: ONV-058.01
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (617) 832-1000
(B) TELEFAX: (617) 832-7000

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 582 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 81..371
- (ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 81..164
- (ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 165..371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGCTTGACC TGCGGCAGTG CAGCCCTTGG GACTTCCCTC GCCTTCCACC TCCTGCTCGT	60
CTGCTTCACA AGCTATCGCT ATG GTG TTC GTG CGC AGG CCG TGG CCC GCC	110
Met Val Phe Val Arg Arg Pro Trp Pro Ala	
-28 -25 -20	
TTG ACC ACA GTG CTT CTG GCC CTG CTC GTC TGC CTA GGG GCG CTG GTC	158
Leu Thr Thr Val Leu Leu Ala Leu Leu Val Cys Leu Gly Ala Leu Val	
-15 -10 -5	
GAC GCC TAC CCC ATC AAA CCC GAG GCT CCC GGC GAA GAC GCC TCG CCG	206
Asp Ala Tyr Pro Ile Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro	
1 5 10	
GAG GAG CTG AAC CGC TAC TAC GCC TCC CTG CGC CAC TAC CTC AAC CTG	254
Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu	
15 20 25 30	
GTC ACC CGG CAG CGG TAT GGG AAA AGA GAC GGC CCG GAC AGG CTT CTT	302
Val Thr Arg Gln Arg Tyr Gly Lys Arg Asp Gly Pro Asp Arg Leu Leu	
35 40 45	
TCC AAA ACG TTC TTC CCC GAC GGC GAG GAC CGC CCC GTC AGG TCG CGG	350
Ser Lys Thr Phe Phe Pro Asp Gly Glu Asp Arg Pro Val Arg Ser Arg	
50 55 60	
TCG GAG GGC CCA GAC CTG TGG TGAGGACCCC TGAGGCCTCC TGGGAGATCT	401
Ser Glu Gly Pro Asp Leu Trp	
65	
GCCAACCACG CCCACGTCAT TTGCATACGC ACTCCCGACC CCAGAAACCC GGATTCTGCC	461
TCCCGACGGC GGCCTCTGGG CAGGGTTCGG GTGCGGCCCT CCGCCCGCGT CTCGGTGCCC	521
CCGCCCCCTG GGCTGGAGGG CTGTGTGTGG TCCTTCCCTG GTCCCAAAT AAAGAGCAAA	581
T	582

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Val Phe Val Arg Arg Pro Trp Pro Ala Leu Thr Thr Val Leu Leu	
-28 -25 -20 -15	
Ala Leu Leu Val Cys Leu Gly Ala Leu Val Asp Ala Tyr Pro Ile Lys	
-10 -5 1	
Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr	
5 10 15 20	
Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr	
25 30 35	
Gly Lys Arg Asp Gly Pro Asp Arg Leu Leu Ser Lys Thr Phe Phe Pro	
40 45 50	

Asp Gly Glu Asp Arg Pro Val Arg Ser Arg Ser Glu Gly Pro Asp Leu
55 60 65

Trp